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(120) Novel polypeptides, cDNA coding these polypeptides and Use thereof

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(151) 1998-04-28

(160) 12

(170) PatentIn Ver. 2.0

(210) 1

(211) 448

(212) PRT

(213) Mus musculus

(400) 1

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-23

-20

-15

-10

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-5

1

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Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr			
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Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly			
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Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr			
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Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala			
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Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val			
75	80	85	
Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val			
90	95	100	105
Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys			
110	115	120	
Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp			
125	130	135	
Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr			
140	145	150	
Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys			
155	160	165	
Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val			
170	175	180	185
Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr			
190	195	200	
Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu			
205	210	215	

4210 · 2

4211 · 1344

4212 · DNA

4213 · *Mus musculus*

4400 · 2

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· 210 · 3

· 211 · 2233

· 212 · DNA

· 213 · Mus musculus

· 220 ·

· 223 · Clone mouse A55 derived from Day 13 mouse embryonic heart

· 220 ·

· 221 · CDS

· 222 · (75).. (1418)

· 220 ·

· 221 · sig_peptide

· 222 · (75).. (143)

· 220 ·

· 221 · mat_peptide

· 222 · (144).. (1418)

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Met Pro Gly Leu Lys Arg Ile Leu Thr Val Thr Ile

-20

-15

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Leu Ala Leu Trp Leu Pro His Pro Gly Asn Ala Gln Gln Gln Cys Thr

-10

-5

-1 1

5

aac ggc ttt gac ctg gac cgc cag tca gga cag tgt cta gat att gat 206
Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp

10

15

20

gaa tgc cgg acc atc cct gag gct tgt cgt ggg gac atg atg tgt gtc 254
Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val

25

30

35

aac cag aat ggc ggg tat ttg tgc atc cct cga acc aac cca gtg tat 302
Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr

40

45

50

cga ggg cct tac tca aat ccc tac tct aca tcc tac tca ggc cca tac 350
Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr

55

60

65

cca gca gcg gcc cca cca gta cca gct tcc aac tac ccc acg att tca 398
Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser

70

75

80

85

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Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln

90	95	100	
tgt gtg gat gtg gac gag tgt gca aca gac tca cac cag tgc aac cct			494
Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro			
105	110	115	
acc cag atc tgt atc aac act gaa gga ggt tac acc tgc tcc tgc acc			542
Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr			
120	125	130	
gat ggg tac tgg ctt ctg gaa ggg cag tgc cta gat att gat gaa tgt			590
Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys			
135	140	145	
cgc tat ggt tac tgc cag cag ctc tgt gca aat gtt cca gga tcc tat			638
Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr			
150	155	160	165
tcc tgt aca tgc aac cct ggt ttc acc ctc aac gac gat gga agg tct			686
Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser			
170	175	180	
tgc caa gat gtg aac gag tgc gaa act gag aat ccc tgt gtt cag acc			734
Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr			
185	190	195	
tgt gtc aac acc tat ggc tct ttc atc tgc cgc tgt gac cca gga tat			782
Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr			
200	205	210	
gaa ctt gag gaa gat ggc att cac tgc agt gat atg gac gag tgc agc			830
Glu Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser			
215	220	225	
ttc tcc gag ttc ctc tgt caa cac gag tgt gtg aac cag ccg ggc tca			878

Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser	
230	245
tac ttc tgc tgc tgc cct cca ggc tac gtc ctg ttg gat gat aac cga	926
Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp Asp Asn Arg	
250	260
agc tgc cag gat atc aat gaa tgt gag cac cga aac cac acg tgt acc	974
Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr	
265	275
tca ctg cag act tgc tac aat cta caa ggg ggc ttc aaa tgt att gat	1022
Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp	
280	290
ccc atc agc tgt gag gag cct tat ctg ctg att ggt gaa aac cgc tgt	1070
Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu Asn Arg Cys	
295	305
atg tgt cct gct gag cac acc agc tgc aga gac cag cca ttc acc atc	1118
Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro Phe Thr Ile	
310	320
ctg tat cgg gac atg gat gtg gtg tca gga cgc tcc gtt cct gct gac	1166
Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp	
330	340
atc ttc cag atg caa gca aca acc cga tac cct ggt gcc tat tac att	1214
Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile	
345	355
ttc cag atc aaa tct ggc aac gag ggt cga gag ttc tat atg cgg caa	1262
Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln	
360	370

aca ggg cct atc agt gcc acc ctg gtg atg aca cgc ccc atc aaa ggg 1310

Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly

375

380

385

cct cgg gac atc cag ctg gac ttg gag atg atc act gtc aac act gtc 1358

Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val

390

395

400

405

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Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser

410

415

420

cag tat ccg ttc tgagcctctg gctaaggcct ctgacactgc ctttcaccag 1458

Gln Tyr Pro Phe

425

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ctgcttgga agacagaggt atccagactg attaaataat tgaagaaaaa aaaaa 2233

210 4

211 423

212 PRT

213 Mus musculus

400 4

Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu
1 5 10 15
Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met
20 25 30
Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn
35 40 45
Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser
50 55 60
Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro
65 70 75 80
Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu
85 90 95
Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln
100 105 110
Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys
115 120 125
Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile
130 135 140
Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro

145	150	155	160
Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp			
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Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys			
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Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp			
	195	200	205
Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp			
	210	215	220
Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln			
225	230	235	240
Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp			
	245	250	255
Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His			
	260	265	270
Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys			
	275	280	285
Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu			
	290	295	300
Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro			
305	310	315	320
Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val			
	325	330	335
Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala			
	340	345	350
Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr			

000221-00000000

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Tyr Val Ser Gln Tyr Pro Phe			
420			

·210· 5

·211· 1269

·212· DNA

·213· Mus musculus

·400· 5

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· 210 · 6

· 211 · 461

· 212 · PRT

· 213 · Mus musculus

· 400 · 6

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-35

-30

-25

Arg Arg Met Ile Leu Thr Val Thr Ile Leu Ala Leu Trp Leu Pro His

-20

-15

-10

-5

Pro Gly Asn Ala Gln Gln Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg

205	210	215	220
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His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro			
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Gly Tyr Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu			
255	260	265	
Cys Glu His Arg Asn His Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn			
270	275	280	
Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro			
285	290	295	300
Tyr Leu Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala Glu His Thr			
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Ser Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val			
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Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr			
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Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn			
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Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr			
365	370	375	380
Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp			
385	390	395	
Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser			
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Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe			

415

420

425

<210 · 7

<211 · 1383

<212 · DNA

<213 · Mus musculus

<400 · 7

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·210· 8

·211· 2429

·212· DNA

·213· Mus musculus

·220·

·223· Clone mouse A55b derived from Day 13 mouse embryonic heart

·220·

·221· CDS

·222· (232).. (1614)

·220·

·221· sig_peptide

·222· (232).. (339)

·220·

<221> mat_peptide

<222> (340)..(1614)

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gactgtctgac tacggcacca gcaattgctt tgcctgcgacg gctgtgagac aagcagaagt 180
ctccgaacac ttctgtctgc gtttgcctcta tgtgtgtgat ttacagaggg a atg gga 237

Met Gly

-35

cct aga agt ttc gag cca atg cac agt gga ctc tgc aga cag aga cgc 285
Pro Arg Ser Phe Glu Pro Met His Ser Gly Leu Cys Arg Gln Arg Arg

-30

-25

-20

atg ata ctc act gtt acc atc ttg gca ctc tgg ctt cca cat cct ggg 333
Met Ile Leu Thr Val Thr Ile Leu Ala Leu Trp Leu Pro His Pro Gly

-15

-10

-5

aat gca cag cag cag tgc aca aac ggc ttt gac ctg gac cgc cag tca 381
Asn Ala Gln Gln Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser

-1 1

5

10

gga cag tgt cta gat att gat gaa tgc cgg acc atc cct gag gct tgt 429
Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys

15

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30

cgt ggg gac atg atg tgt gtc aac cag aat ggc ggg tat ttg tgc atc 477
Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile

35

40

45

cct cga acc aac cca gtg tat cga ggg cct tac tca aat ccc tac tct 525

Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser	
50 55 60	
aca tcc tac tca ggc cca tac cca gca ggc gcc cca cca gta cca gct	573
Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala	
65 70 75	
tcc aac tac ccc acg att tca agg cct ctt gtc tgc cgc ttt ggg tat	621
Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr	
80 85 90	
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Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr	
95 100 105 110	
gac tca cac cag tgc aac cct acc cag atc tgt atc aac act gaa gga	717
Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly	
115 120 125	
ggt tac acc tgc tcc tgc acc gat ggg tac tgg ctt ctg gaa ggg cag	765
Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln	
130 135 140	
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Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys	
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Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr	
160 165 170	
ctc aac gac gat gga agg tct tgc caa gat gtg aac gag tgc gaa act	909
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195

200

205

tgc cgc tgt gac cca gga tat gaa ctt gag gaa gat ggc att cac tgc 1005

Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile His Cys

210

215

220

agt gat atg gac gag tgc agc ttc tcc gag ttc ctc tgt caa cac gag 1053

Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu

225

230

235

tgt gtg aac cag cag ggc tca tac ttc tgc teg tgc cct cca ggc tac 1101

Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr

240

245

250

gtc ctg ttg gat gat aac cga agc tgc cag gat atc aat gaa tgt gag 1149

Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu

255

260

265

270

cac cga aac cac acg tgt acc tca ctg cag act tgc tac aat cta caa 1197

His Arg Asn His Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln

275

280

285

ggg ggc ttc aaa tgt att gat ccc atc agc tgt gag gag cct tat ctg 1245

Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu

290

295

300

ctg att ggt gaa aac cgc tgt atg tgt cct gct gag cac acc agc tgc 1293

Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys

305

310

315

aga gac cag cca ttc acc atc ctg tat cgg gac atg gat gtg gtg tca 1341

Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser

320	325	330	
gga cgc tcc gtt cct gct gac atc ttc cag atg caa gca aca acc cga	1389		
Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg			
335	340	345	350
tac cct ggt gcc tat tac att ttc cag atc aaa tct ggc aac gag ggt	1437		
Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly			
355	360	365	
cga gag ttc tat atg cgg caa aca ggg cct atc agt gcc acc ctg gtg	1485		
Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val			
370	375	380	
atg aca cgc ccc atc aaa ggg cct cgg gac atc cag ctg gac ttg gag	1533		
Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu			
385	390	395	
atg atc act gtc aac act gtc atc aac ttc aga ggc agc tcc gtg atc	1581		
Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile			
400	405	410	
cga ctg cgg ata tat gtg tcg cag tat ccg ttc tgagcctctg gctaaggcct	1634		
Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe			
415	420	425	
ctgacactgc ctttcaccag caccgagggga cgggaggaga aaggaaacca gcaagaatga	1694		
gagcgagaca gacattgcac ctttctctgct gaatatctcc tggggggcacc agcctagcat	1754		
cttgacccat atctgtacta ttgcagatgg tcactctgaa ggacacctg ccttcagttc	1814		
ctatgatgca gttatecaaaa agtgtttcacc ttagcccttg atatgagggt gccagtgact	1874		
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ctgggaatag ctatgttget tcttgcatgt tetgagaagg ctatgggaac acaccacage 2114
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 tgaagaaaaa aaaaa 2429

· 210 · 9

· 211 · 423

· 212 · PRT

· 213 · Mus musculus

· 400 · 9

Gln	Cys	Thr	Asn	Gly	Phe	Asp	Leu	Asp	Arg	Gln	Ser	Gly	Gln	Cys	Leu
1				5					10				15		
Asp	Ile	Asp	Glu	Cys	Arg	Thr	Ile	Pro	Glu	Ala	Cys	Arg	Gly	Asp	Met
			20						25				30		
Met	Cys	Val	Asn	Gln	Asn	Gly	Gly	Tyr	Leu	Cys	Ile	Pro	Arg	Thr	Asn
			35				40						45		
Pro	Val	Tyr	Arg	Gly	Pro	Tyr	Ser	Asn	Pro	Tyr	Ser	Thr	Ser	Tyr	Ser
			50				55					60			
Gly	Pro	Tyr	Pro	Ala	Ala	Ala	Pro	Pro	Val	Pro	Ala	Ser	Asn	Tyr	Pro
			65				70					75			80
Thr	Ile	Ser	Arg	Pro	Leu	Val	Cys	Arg	Phe	Gly	Tyr	Gln	Met	Asp	Glu

	85	90	95
Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln			
100	105	110	
Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys			
115	120	125	
Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile			
130	135	140	
Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro			
145	150	155	160
Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp			
165	170	175	
Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys			
180	185	190	
Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp			
195	200	205	
Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp			
210	215	220	
Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln			
225	230	235	240
Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp			
245	250	255	
Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His			
260	265	270	
Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys			
275	280	285	
Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu			

290 295 300
 Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro
 305 310 315 320
 Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val
 325 330 335
 Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala
 340 345 350
 Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr
 355 360 365
 Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro
 370 375 380
 Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val
 385 390 395 400
 Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile
 405 410 415
 Tyr Val Ser Gln Tyr Pro Phe
 420

·210· 10

·211· 1269

·212· DNA

·213· Mus musculus

·400· 10

cagtcacaaa acggctttga cctggaccgc cagtcaggac agtgtctaga tattgatgaa 60

<220>

<223> Description of Artificial Sequence:Primer

<400> 11

cgattgaatt ctagacctgc ctgagnnnn nnnnn

35

· 210 · 12

· 211 · 27

· 212 · DNA

· 213 · Artificial Sequence

· 220 ·

<223> Description of Artificial Sequence:mA55 R1 primer

<400> 12

cgtttgtgca ctgctgctgt gcattcc

27